



SEQUENCE LISTING

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JUL 19 2002

TECH CENTER 1600/2900

<110> BARCHIESI, Rino
DEL GIUDICE, Giuseppe
RAPPUOLI, Rino

<120> DETOXIFIED MUTANTS OF BACTERIAL ADP-RIBOSYLATING TOXINS
AS PARENTERAL ADJUVANTS

<130> 2302-1393 / PP01393.002

<140> 09/044,696

<141> 1998-03-18

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(708)

<220>

<223> Description of Artificial Sequence: wild-type Subunit
A from E. coli heat labile toxin

<400> 1

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Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
1 5 10 15

aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga 96
Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
20 25 30

gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa 144
Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
35 40 45

acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt 192
Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
50 55 60

ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca 240
Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
65 70 75 80

ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta 288
Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
85 90 95

att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta 336
Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu

100 105 110
 ggt gga ata cca tat tct cag ata tat gga tgg tat cgt gtt aat ttt 384
 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
 115 120 125
 ggt gtg att gat gaa cga tta cat cgt aac agg gaa tat aga gac cgg 432
 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
 130 135 140
 tat tac aga aat ctg aat ata gct ccg gca gag gat ggt tac aga tta 480
 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
 145 150 155 160
 gca ggt ttc cca ccg gat cac caa gct tgg aga gaa gaa ccc tgg att 528
 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
 165 170 175
 cat cat gca cca caa ggt tgt gga gat tca tca aga aca atc aca ggt 576
 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
 180 185 190
 gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc agg 624
 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
 195 200 205
 gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag tca 672
 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
 210 215 220
 gag gtt gac ata tat aac aga att cgg gat gaa tta tga 711
 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
 225 230 235

<210> 2

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: wild-type Subunit
A from E. coli heat labile toxin

<400> 2

Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
1 5 10 15

Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
20 25 30

Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
35 40 45

Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
50 55 60

Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser

65		70		75		80									
Leu	Thr	Ile	Tyr	Ile	Val	Ile	Ala	Asn	Met	Phe	Asn	Val	Asn	Asp	Val
				85					90					95	
Ile	Ser	Val	Tyr	Ser	Pro	His	Pro	Tyr	Glu	Gln	Glu	Val	Ser	Ala	Leu
		100						105					110		
Gly	Gly	Ile	Pro	Tyr	Ser	Gln	Ile	Tyr	Gly	Trp	Tyr	Arg	Val	Asn	Phe
		115					120					125			
Gly	Val	Ile	Asp	Glu	Arg	Leu	His	Arg	Asn	Arg	Glu	Tyr	Arg	Asp	Arg
	130					135					140				
Tyr	Tyr	Arg	Asn	Leu	Asn	Ile	Ala	Pro	Ala	Glu	Asp	Gly	Tyr	Arg	Leu
145				150						155					160
Ala	Gly	Phe	Pro	Pro	Asp	His	Gln	Ala	Trp	Arg	Glu	Glu	Pro	Trp	Ile
			165						170					175	
His	His	Ala	Pro	Gln	Gly	Cys	Gly	Asp	Ser	Ser	Arg	Thr	Ile	Thr	Gly
		180						185					190		
Asp	Thr	Cys	Asn	Glu	Glu	Thr	Gln	Asn	Leu	Ser	Thr	Ile	Tyr	Leu	Arg
	195						200					205			
Glu	Tyr	Gln	Ser	Lys	Val	Lys	Arg	Gln	Ile	Phe	Ser	Asp	Tyr	Gln	Ser
	210					215					220				
Glu	Val	Asp	Ile	Tyr	Asn	Arg	Ile	Arg	Asp	Glu	Leu				
225					230					235					

Sub
E31

<210> 3
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(720)

<220>
 <223> Description of Artificial Sequence: wild-type CT subunit A

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Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile	
1 5 10 15	
aag cag tca ggt ggt ctt atg cca aga gga cag agt gag tac ttt gac	96
Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp	
20 25 30	
cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act	144
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr	
35 40 45	

cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att 192
 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
 50 55 60
 agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat 240
 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
 65 70 75 80
 tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac 288
 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
 85 90 95
 gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa 336
 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
 100 105 110
 gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat 384
 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
 115 120 125
 cga gtt cat ttt ggg ggt ctt gat gaa caa tta cat cgt aat agg ggc 432
 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
 130 135 140
 tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat 480
 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
 145 150 155 160
 ggt tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa 528
 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
 165 170 175
 gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga 576
 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
 180 185 190
 tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta 624
 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
 195 200 205
 aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca 672
 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
 210 215 220
 ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta 720
 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
 225 230 235 240
 tga 723

<210> 4

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: wild-type CT

subunit A

<400> 4

Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
1 5 10 15
Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
20 25 30
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
35 40 45
Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
50 55 60
Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
65 70 75 80
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
85 90 95
Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
100 105 110
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
115 120 125
Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
130 135 140
Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
145 150 155 160
Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
165 170 175
Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
180 185 190
Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
195 200 205
Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
210 215 220
Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
225 230 235 240

<210> 5

<211> 240

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: wild-type Subunit
A from E. coli heat labile toxin

<400> 5

Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
1 5 10 15
Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr Phe Asp
20 25 30
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
35 40 45
Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu
50 55 60
Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Gly Tyr
65 70 75 80
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
85 90 95
Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Gln Glu
100 105 110
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
115 120 125
Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
130 135 140
Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
145 150 155 160
Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
165 170 175
Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
180 185 190
Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
195 200 205
Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
210 215 220
Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
225 230 235 240

Sub
E21